WHAT IS CLAIMED IS:

1. A set of nucleic acids comprising:

a first pair of primers, each containing an oligo-nucleotide selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 2, and

a second pair of primers, each containing an oligo-nucleotide selected from the hexon gene region of adenovirus,

wherein each oligo-nucleotide has 14-40 nucleotides in length.

2. The set of nucleic acids of claim 1, further comprising:

a third pair of primers, each containing an oligo-nucleotide specific for human parainfluenza virus 1;

a fourth pair of primers, each containing an oligo-nucleotide specific for human parainfluenza virus 3;

a fifth pair of primers, each containing an oligo-nucleotide specific for respiratory syncytial virus;

a sixth pair of primers, each containing an oligo-nucleotide specific for influenza virus A; or

a seventh pair of primers, each containing an oligo-nucleotide specific for influenza virus B;

or a combination thereof.

3. The set of nucleic acids of claim 2, wherein

the oligo-nucleotides in the third pair of primers are selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 1,

the oligo-nucleotides in the fourth pair of primers are selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 3,

the oligo-nucleotides in the fifth pair of primers are selected from the non-structural protein 2 gene region of respiratory syncytial virus,

the oligo-nucleotides in the sixth pair of primers are selected from the non-structural protein gene region of influenza virus A, and

the oligo-nucleotides in the seventh pair of primers are selected from the hemagglutinin-neuraminidase gene region of influenza virus B.

4. The set of nucleic acids of claim 1, wherein

the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:5 and 7, or SEQ ID NOs:6 and 7; and

the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27.

5. The set of nucleic acids of claim 4, further comprising:

a third pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:1 and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;

a fourth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:8 and 10, SEQ ID NOs:8 and 11, or SEQ IN NOs:9 and 11;

a fifth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:12 and 14, or SEQ ID NOs:13 and 15;

a sixth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs: 16 and 18, or SEQ ID NOs:17 and 19; or

a seventh pair of primers containing, respectively, oligo-nucleotides SEQ ID NO:20 and 22, or SEQ ID NOs:21 and 23,

or a combination thereof.

6. A set of nucleic acids comprising:

a first nucleic acid obtained from amplification of a respiratory syncytial virus nucleic acid template with a first pair of primers, each containing an oligo-nucleotide selected from the non-structural protein 2 gene region;

a second nucleic acid obtained from amplification of an influenza virus A nucleic acid template with a second pair of primers, each containing an oligo-nucleotide selected from the non-structural protein gene region; or

a third nucleic acid obtained from amplification of an influenza virus B nucleic acid template with a third pair of primers, each containing an oligo-nucleotide selected from the hemagglutinin-neuraminidase gene region,

or a combination thereof,

wherein each oligo-nucleotide has 14-40 nucleotides in length.

7. The set of nucleic acids of claim 6, wherein

the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:12 and 14, or SEQ ID NOs:13 and 15;

the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID NOs: 16 and 18, or SEQ ID NOs:17 and 19; and

the oligo-nucleotides in the third pair of primers are, respectively, SEQ ID NOs:20 and 22, or SEQ ID NOs:21 and 23.

8. The set of nucleic acids of claim 7, further comprising:

a fourth nucleic acid obtained from amplification of a human parainfluenza virus 1 nucleic acid template with a fourth pair of primers, said fourth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:1 and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;

a fifth nucleic acid obtained from amplification of a human parainfluenza virus 2 nucleic acid template with a fifth pair of primers, said fifth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:5 and 7, or SEQ ID NOs:6 and 7;

a sixth nucleic acid obtained from amplification of a human parainfluenza virus 3 nucleic acid template with a sixth pair of primers, said sixth pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:8 and 10, SEQ ID NOs:8 and 11, or SEQ IN NOs:9 and 11; or

a seventh nucleic acid obtained from amplification of an adenovirus nucleic acid template with a seventh pair of primers, said seventh pair of primers containing, respectively, oligo-nucleotides SEQ ID NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27;

or a combination thereof.

9. A set of nucleic acids comprising:

a first nucleic acid containing a first oligo-nucleotide selected from the non-structural protein 2 gene region of respiratory syncytial virus,

a second nucleic acid containing a second oligo-nucleotide selected from the non-structural protein gene region of influenza virus A, or

a third nucleic acid containing a third oligo-nucleotide selected from the hemagglutinin-neuraminidase gene region of influenza virus B,

or a combination thereof,

wherein each nucleic acid has 20-1,000 nucleotides in length.

10. The set of nucleic acids of claim 9, wherein each nucleic acid has 20-500 nucleotides in length.

11. The set of nucleic acids of claim 10, wherein each nucleic acid has 20-50 nucleotides in length.

12. The set of nucleic acids of claim 9, wherein each oligo-nucleotide is selected from the group consisting of SEQ ID NOs:40-52 and sequences complementary thereto.

13. The set of nucleic acids of claim 12, wherein each nucleic acid has 20-500 nucleotides in length.

14. The set of nucleic acids of claim 13, wherein each nucleic acid has 20-50 nucleotides in length.

15. The set of nucleic acids of claim 12, further comprising a nucleic acid containing an oligo-nucleotide selected from the group consisting of SEQ ID NOs:28-39, 53-57, and sequences complementary thereto, wherein each nucleic acid has 20-1,000 nucleotides in length.

16. The set of nucleic acids of claim 15, wherein each nucleic acid has 20-500 nucleotides in length.

17. The set of nucleic acids of claim 16, wherein each nucleic acid has 20-50 nucleotides in length.

18. A method of simultaneously detecting viruses which cause respiratory infections comprising:

providing a nucleic acid from a sample suspected of containing a virus to be detected;

amplifying the nucleic acid with a set of primers specific for a group of target viruses, said set of primers containing a first pair of primers, each having an oligo-nucleotide selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 2, and a second pair of primers, each having an oligo-nucleotide selected from the hexon gene region of adenovirus, each oligo-nucleotide having 14-40 nucleotides in length; and

detecting amplification products;

whereby detection of an amplification product specific for a target virus indicates the presence of the target virus.

19. The method of claim 18, wherein, in the amplifying step, said set of primers further containing:

a third pair of primers, each including an oligo-nucleotide specific for human parainfluenza virus 1,

a fourth pair of primers, each including an oligo-nucleotide specific for human parainfluenza virus 3,

a fifth pair of primers, each including an oligo-nucleotide specific for respiratory syncytial virus,

a sixth pair of primers, each including an oligo-nucleotide specific for influenza virus A, or

a seventh pair of primers, each including an oligo-nucleotide specific for influenza virus B,

or a combination thereof.

20. The method of claim 19, wherein

the oligo-nucleotides in the third pair of primers are selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 1,

the oligo-nucleotides in the fourth pair of primers are selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 3,

the oligo-nucleotides in the fifth pair of primers are selected from the non-structural protein 2 gene region of respiratory syncytial virus,

the oligo-nucleotides in the sixth pair of primers are selected from the non-structural protein gene region of influenza virus A, and

the oligo-nucleotides in the seventh pair of primers are selected from the hemagglutinin-neuraminidase gene region of influenza virus B.

21. The method of claim 18, wherein

the oligo-nucleotides in the first pair of primers are, respectively, SEQ ID NOs:5 and 7, or SEQ ID NOs:6 and 7; and

the oligo-nucleotides in the second pair of primers are, respectively, SEQ ID NOs:24 and 26, SEQ ID NOs:24 and 27, or SEQ ID NOs:25 and 27.

22. The method of claim 21, wherein said set of primers further containing:

a third pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:1 and 3, SEQ ID NOs:2 and 3, or SEQ ID NOs:1 and 4;

a fourth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:8 and 10, SEQ ID NOs:8 and 11, or SEQ IN NOs:9 and 11;

a fifth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs:12 and 14, or SEQ ID NOs:13 and 15;

a sixth pair of primers including, respectively, oligo-nucleotides SEQ ID NOs: 16 and 18, or SEQ ID NOs:17 and 19; or

a seventh pair of primers including, respectively, oligo-nucleotides SEQ ID NO:20 and 22, or SEQ ID NOs:21 and 23;

or a combination thereof.

23. The method of claim 18, wherein the detecting step includes hybridizing the amplification product to a set of probes, said set of probes containing:

a first probe having a first nucleic acid selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 2, and

a second probe having a second nucleic acid selected from the hexon gene region of adenovirus,

each probe having 20-2000 nucleotides in length.

24. The method of claim 23, wherein each nucleic acid is selected from the group consisting of SEQ ID NOs:34-36 and 53-57.

25. The method of claim 19, wherein the detecting step includes hybridizing the amplification product to a set of primers, said set of probes contains:

a first probe having a first nucleic acid selected from the hemagglutinin-neuraminidase gene region of human parainfluenza virus 2, and

a second probe having a second nucleic acid selected from the hexon gene region of adenovirus;

said set of probes further contains:

a third probe having a third nucleic acid specific for human parainfluenza virus 1,

a fourth probe having a fourth nucleic acid specific for human parainfluenza virus 3,

a fifth probe having a fifth nucleic acid specific for respiratory syncytial virus,

a sixth probe having a sixth nucleic acid specific for influenza virus A, or

a seventh probe having a seventh nucleic acid specific for influenza virus B,

or a combination thereof;

each probe having 20-2000 nucleotides in length.

26. The method of claim 25, wherein each probe is selected from the group consisting of SEQ ID NOs:28-57.